Amendments to the Claims:

The following list of claims will replace all prior versions of the claims in the application:

1. (*Canceled*)

2. (*Currently amended*) A method for assessing toxicity of a compound of interest, comprising:

exposing tissue samples comprising a set of genes to the compound of interest;

measuring the hybridization signal of each gene in the set of genes;

creating gene expression profiles using a plurality of variables, wherein the plurality of variables includes time and dose;

identifying patterns within the gene expression profiles that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression progresses in a same direction with time and increased dose and does not change direction at adjacent time points, and selecting a plurality of gene expression profiles that fit the patterns;

creating one or more composite variables from the selected gene expression profiles;

creating ~~one~~ a single predictive composite from the composite variables, wherein the one predictive composite comprises a binary value indicating one of a positive or negative toxicological response to the compound of interest.

3. (*Previously presented*) The method of Claim 2, wherein the set of genes comprises 10-100,000 genes.

4. (*Previously presented*) The method of Claim 2, wherein the plurality of variables further includes treatment.

5. (*Canceled*)

6. (*Previously presented*) The method of Claim 2, wherein the step of measuring further comprises averaging the hybridization signals of a portion of the genes having a lowest signal intensity to determine a background level; and

selecting for further analysis the hybridization signals having a difference signal intensity that exceeds the background level, wherein the difference signal intensity is taken relative to a mismatch control for each gene.

7. (*Previously presented*) The method of Claim 2, wherein the step of identifying comprises performing contrast analysis.

8. (*Previously presented*) The method of Claim 2, wherein the step of identifying comprises performing cluster analysis.

9. (*Previously presented*) The method of Claim 2, wherein the step of creating one or more composite variables comprises performing principal components analysis.

10. (*Currently amended*) The method of Claim 2, wherein the ~~one~~ single predictive composite is created using logistic regression or discriminant analysis.

11. -22. (*Canceled*)

23. (*Previously presented*) The method of Claim 2, wherein the step of creating one or more composite variables comprises performing partial least squares analysis.

24. (*Previously presented*) The method of Claim 2, wherein the step of creating one or more composite variables comprises performing factor analysis.

25. (*Previously presented*) The method of Claim 2, wherein the compound of interest is acetaminophen.

26. (*Currently Amended*) A method for assessing the toxicity of a compound of interest, comprising:

exposing tissues comprising a set of genes to the compound of interest;

generating gene expression data corresponding to a hybridization signal of each gene in the set of genes;

identifying patterns in the gene expression data that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression progresses in a same direction with time and increased dose and does not change direction at adjacent time points, and selecting a subset of the gene expression data that fit the patterns, wherein the subset comprises a plurality of genes;

defining one or more composite variables using the subset of the gene expression data; and

converting the one or more composite variables into ~~one~~ a single predictive composite measure for determining a probability of similarity;

wherein the probability of similarity comprises an indicator of toxicological effect of the compound of interest.

27. (*Previously presented*) The method of claim 26, wherein the step of identifying comprises performing contrast analysis.

28. (*Previously presented*) The method of claim 26, where the step of defining one or more composite variables comprises performing principal components analysis.

29. (*Previously presented*) The method of claim 28, wherein the step of converting comprises performing a logistic regression using the principal components identified in the principal components analysis.

30. (*Previously presented*) The method of claim 26, wherein the tissues are liver, kidney, brain, spleen, pancreas and lung.

31. (*Previously presented*) The method of claim 26, wherein the step of generating gene expression data further comprises averaging the hybridization signals of a portion of the genes having a lowest signal intensity to determine a background level; and

selecting for further analysis the hybridization signals having a difference signal intensity that exceeds the background level, wherein the difference signal intensity is taken relative to a mismatch control gene for each gene.

32. (*Previously presented*) The method of Claim 2, wherein the tissue samples are liver, kidney, brain, spleen, pancreas and lung.

33. (*Previously presented*) The method of Claim 2, wherein the compound of interest is CCl_4.

34. (*Currently amended*) A method for assessing the toxicity of a compound of interest, comprising:

exposing tissues comprising a set of genes to the compound of interest;

generating gene expression data corresponding to a hybridization intensity of each gene in the set of genes;

performing analysis of variants to identify patterns in the gene expression data that demonstrate time stability and dose dependence, wherein a pattern is defined where a change in gene expression progresses in a same direction with time and increased dose and does not change direction at adjacent time points;

selecting a subset of gene expression data that fits the patterns, wherein the subset comprises a plurality of genes;

applying factor analysis to the subset of gene expression data to define one or more composite variables; and

applying logistic regression to convert the one or more composite variables into ~~one~~ a single predictive composite measure of toxicological effect of the compound of interest.

35. (*Previously presented*) The method of claim 34, where the step of performing an analysis of variants comprises analyzing time stability and dose dependence simultaneously.

36. (*Previously presented*) The method of claim 34, wherein the step of performing an analysis of variants comprises cluster analysis or contrast analysis.

37. (*Previously presented*) The method of claim 34, wherein the step of applying factor analysis comprises performing principal components analysis or least squares analysis.